

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
- (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/842,385
(B) FILING DATE: 23-APR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6084.US.P1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 847/935-1729
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCGCATCCG	AGCCATGGCC	CAGCAGGTGT	TTATGCTGGA	CACCCAGTGC	TCACCAAAGA	60
CACCAAACAA	CTTTGACCAC	GCTCAGTCCT	GCCAGCTCAT	TATTGAGCTG	CCTCCTGATG	120
AAAAACCAAA	TGGACACACC	AAGAAAAGCG	TGTCTTTTCAG	GGAAATTGTG	GTGAGCCTGC	180
TGTCTCATCA	GGTGTACTC	CAGAACTTAT	ATGACATCTT	GTTAGAAGAG	TT	232

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTTTCAGGGA	AATTGTGGTG	AGCCTGCTGT	CTCATCAGGT	GTTACTCCAG	AACTTATATG	60
ACATCTTGTT	AGAAGAGTTT	GTCAAAGGCC	CCTCTCCTGG	AGAGGAAAAG	ACGATACAAG	120
TGCCAGAAGC	CAAGCTGGCT	GGCTTCCTCA	GATACATCTC	TATGCAGAAC	TTGGCAGTCA	180
TATTTCGACCT	GCTGCTGGAC	TCTTATAGGA	CTGCCAGGGA	GTTTGACACC	AGCCCCGGGC	240
TGAAGTGCCT	GCTGAAGAAA	GTGTCTGGCA	TCGGGGGCGC	CGCCAACCT		289

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCAGTCATA	TTCGACCTGC	TGCTGGACTC	TTATAGGACT	GCCAGGGAGT	TTGACACCAG	60
CCCCGGGCTG	AAGTGCCTGC	TGAAGAAAGT	GTCTGGCATC	GGGGGCGCCG	CCAACCTCTA	120
CCGCCAGTCT	GCGATGAGTT	TAACATTTAT	TTCCACGCCC	TGGTGTGTGC	TGTTCTCACC	180
AATCAAGAAA	ACATCACGGC	CGAGCAAGTG	AAGAAGGTCC	TTTTTGAGGA	CGACGAGAGA	240
AGCACGGATT	CTTCCCAGCA	GTGT				264

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATATTTCGAC	CTGCTGCTGG	ACTCTTATAG	GA CTGCCAGG	GAGTTTGACA	CCAGCCCCGG	60
GCTGAAGTGC	CTGCTGAAGA	AAGTGTCTGG	CATCGGGGGC	GCCGCCAACC	TCTACCGCCA	120
GTCTGCGATG	AGCTTTAACA	TTTATTTCCA	CGCCCTGGTG	TGTGCTGTTT	TCACCAATCA	180
AGAAACCATC	ACGGCCGAGC	AAGTGAAGAA	GGTCCTTTTT	GAGGACGACG	AGAGAAGCAC	240
GGATTCTTCC	CAGCAGTGTT					260

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCACTGGGTC	CCAGGGGCCA	GGACTCCCCG	CTGCTTCAGC	GTCCCCAGCA	CTTGATGGAC	60
CAAGGGCAAA	TGCGGCATTC	CTTCAGCGCA	GGCCCCGAGC	TGCTGCGACA	GGACAAGAGG	120
CCCCGCTCAG	GCTCCACCGG	GAGCTCCCTC	AGTGTCTCGG	TGAGAGACGC	AGAAGCACAG	180
ATCAGGCATG	GACCAACAT					199

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATTCTTTCA	GCGCAGGCC	CGAGCTGCTG	CGACAGGACA	AGAGGCCCCG	CTCAGGCTCC	60
ACCGGGAGCT	CCCTCAGTGT	CTCGGTGAGA	GACGCAGAAG	CACAGATCCA	GGCATGGACC	120
AACATGGTGC	TAACAGTTCT	CAATCAGATT	CAGATTCTCC	CAGACCAGAC	CTTCACGGCC	180
CTCCAGCCCCG	CAGTGTTC	GTGCATCAGT	CAGCTGACCT	GTCACGTGAC	CGACATCAGA	240
GTTCGCCAGG	CTGCGAGGGA	GTGGCTGGGC	AGGGTGGGCC	GTGTCTATGA	CATCATTTGT	300
TAGCCGACTC	CTGTTCTACT	CTCCCACCAA	ATAACAGTAG	TGAGGGTTAG	AGTCCTGCCA	360
ATACAGCTGT	TGCATTTTCC	CCACCACCTAG	CCCCACTTAA	ACTACTACTA	CTGTCTCAGA	420
GAACAGTGTT	TCCTAATGTA	AAAAGCCTTT	CCAACCCTG	ATCAGCATTA		470

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACGGCCCTC	CAGCCCGCAG	TGTTCCCGTG	CATCAGTCAG	CTGACCTGTC	ACGTGACCGA	60
CATCAGAGTT	CGCCAGGCTG	TGAGGGAGTG	GCTGGGCAGG	GTGGGCCGTG	TCTATGACAT	120
CATTGTGTAG	CCGACTCCTG	TTCTACTCTC	CCACCAAATA	ACAGTAGTGA	GGGTTAGAGT	180
CCTGCCAATA	CAGCTGTTGC	ATTTTCCCCA	CCACTAGCCC	CACTTAAACT	AC	232

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAGGTTTGT	ATCTAGATGA	CACAAACGAT	ATTCTGATTT	TGCACATTAT	TATAGAAGAA	60
TCTATAATCC	TTGATATGTT	TCTAACTCTT	GAAGTATATT	TCCCAGTGCT	TTTGCTTACA	120

GTGTTGTC	CAAATGGGTC	ATTTTCAAGG	ATTACTCATT	TGAAAACACT	ATATTGATCC	180
ATTTGATCCA	TCATTTAAAA	AATAAATACA	ATTCCTAAGG	CAATATCTGC	TGGTAAGTCA	240
AGCT						244

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCAGTCATA	TTTCGACCTGC	TGCTGGACTC	TTATAGGACT	GCCAGGGAGT	TTGACACCAG	60
CCCCGGGCTG	AAGTGCCTGC	TGAAGAAAGT	GTCTGGCATC	GGGGGCGCCG	CCAACCTCTA	120
CCGCCAGTCT	GCGATGAGCT	TTAACATTTA	TTTCCACGCC	CTGGTGTGTG	CTGTTCTCAC	180
CAATCAAGAA	ACCATCACGG	CCGAGCAAGT	GAAGAAGGTC	CTTTTTGAGG	ACGACGAGAG	240
AAGCACGGAT	TCTTCCCAGC	AGTGTTTCATC	TGAGGATGAA	GACATCTTTG	AGGAAACCGC	300
CCAGGTCAGC	CCCCCGAGAG	GCAAGGAGAA	GAGACAGTGG	CGGGCACGGA	TGCCCTTGCT	360
CAGCGTCCAG	CCTGTCCAGC	ACGCAGATTG	GGTGTGGCTG	GTCAAGAGGC	TGCACAAGCT	420
GTGCATGGAA	CTGTGCAACA	ACTACATCCA	GATGCACTTG	GACCTGGAGA	ACTGTATGGA	480
GGAGCCTCCC	ATCTTCAAGG	GCGACCCGTT	CTTCATCCTG	CCCTCCTTCC	AGTCCGAGTC	540
ATCCACCCCA	TCCACCGGGG	GCTTCTCTGG	GAAAGAAACC	CCTTCCGAGG	ATGACAGAAG	600
CCAGTCCCGG	GAGCACATGG	GCGAGTCCCT	GAGCCTGAAG	GCCGGTGGTG	GGGACCTGCT	660
GCTGCCCCCC	AGCCCCAAAG	TGGAGAAGAA	GGATCCCAGC	CGGAAGAAGG	AGTGGTGGGA	720
GAATGCGGGG	AACAAAATCT	ACACCATGGC	AGCCGACAAG	ACCATTTCAA	AGTTGATGAC	780
CGAATACAAA	AAGAGGAAAC	AGCAGCACAA	CCTGTCCGCG	TTCCCCAAAG	AGGTCAAAGT	840
GGAGAAGAAA	GGAGAGCCAC	TGGGTCCCAG	GGGCCAGGAC	TCCCCGCTGC	TTCAGCGTCC	900
CCAGCACTTG	ATGGACCAAG	GGCAAATGCG	GCATTCCTTC	AGCGCAGGCC	CCGAGCTGCT	960
GCGACAGGAC	AAGAGGCCCC	GCTCAGGCTC	CACCGGGAGC	TCCCTCAGTG	TCTCGGTGAG	1020
AGACGCAGAA	GCACAGATCC	AGGCATGGAG	CAACATGGTG	CTAACAGTTC	TCAATCAGAT	1080
TCAGATTCTC	CCAGACCAGA	CCTTCACGGC	CCTCCAGCCC	GCAGTGTTC	CGTGCATCAG	1140
TCAGCTGACC	TGTCACGTGA	CCGACATCAG	AGTTCGCCAG	GCTGTGAGGG	AGTGGCTGGG	1200
CAGGGTGGGC	CGTGTCTATG	ACATCATTGT	GTAGCCGACT	CCTGTTCTAC	TCTCCCACCA	1260
AATAACAGTA	GTGAGGGTTA	GAGTCCTGCC	AATACAGCTG	TTGCATTTTC	CCCACCACTA	1320
GCCCCACTTA	AACTACTACT	ACTGTCTCAG	AGAACAGTGT	TTCTTAATGT	AAAAAGCCTT	1380
TCCAACCACT	GATCAGCATT	GGGGCCATAC	TAAGGTTTGT	ATCTAGATGA	CACAAACGAT	1440
ATTCTGATTT	TGCACATTAT	TATAGAAGAA	TCTATAATCC	TTGATATGTT	TCTAACTCTT	1500
GAAGTATATT	TCCCAGTGCT	TTTGCTTACA	GTGTTGTCCC	CAAATGGGTC	ATTTTCAAGG	1560
ATTACTCATT	TGAAAACACT	ATATTGATCC	ATTTGATCCA	TCATTTAAAA	AATAAATACA	1620
ATTCCTAAGG	CAATATCTGC	TGGTAAGTCA	AGCTGATAAA	CACTCAGACA	TCTAGTACCA	1680
GGGATTATTA	ATTGGAGGAA	GATTTATGGT	TATGGGTCTG	GCTGGGAAGA	AGACAACTAT	1740
AAATACATAT	TCTTGGGTGT	CATAATCAAG	A			1771

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2096 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCGCATCCG	AGCCATGGCC	CAGCAGGTGT	TTATGCTGGA	CACCCAGTGC	TCACCAAAGA	60
CACCAAACAA	CTTTGACCAC	GCTCAGTCCT	GCCAGCTCAT	TATTGAGCTG	CCTCCTGATG	120
AAAAACCAAA	TGGACACACC	AAGAAAAGCG	TGTCTTTCAG	GGAAATTGTG	GTGAGCCTGC	180
TGTCTCATCA	GGTGTTACTC	CAGAAGTTAT	ATGACATCTT	GTTAGAAGAG	TTTGTCAAAG	240
GCCCCCTCTC	TGGAGAGGAA	AAGACGATAC	AAGTGCCAGA	AGCCAAGCTG	GCTGGCTTCC	300
TCAGATACAT	CTCTATGCAG	AACTTGGCAG	TCATATTGCA	CCTGCTGCTG	GACTCTTATA	360
GGACTGCCAG	GGAGTTTGAC	ACCAGCCCCG	GGCTGAAGTG	CCTGCTGAAG	AAAGTGCTCTG	420
GCATCGGGGG	CGCCGCCAAC	CTCTACCGCC	AGCTTGCGAT	GAGCTTTAAC	ATTTATTTCC	480
ACGCCCTGGT	GTGTGCTGTT	CTCACCATC	AAGAAACCAT	CACGGCCGAG	CAAGTGAAGA	540

AGGTCCTTTT	TGAGGACGAC	GAGAGAAGCA	CGGATTCTTC	CCAGCAGTGT	TCATCTGAGG	600
ATGAAGACAT	CTTTGAGGAA	ACCGCCAGG	TCAGCCCCC	GAGAGGCAAG	GAGAAGAGAC	660
AGTGGCGGGC	ACGGATGCCC	TTGCTCAGCG	TCCAGCCTGT	CAGCAACGCA	GATTGGGTGT	720
GGCTGGTCAA	GAGGCTGCAC	AAGCTGTGCA	TGGAAGTGTG	CAACAACACT	ATCCAGATGC	780
ACTTGGACCT	GGAGAACTGT	ATGGAGGAGC	CTCCCATCTT	CAAGGGCGAC	CCGTTCTTCA	840
TCCTGCCCTC	CTTCCAGTCC	GAGTCATCCA	CCCCATCCAC	CGGGGGCTTC	TCTGGGAAAG	900
AAACCCCTTC	CGAGGATGAC	AGAAGCCAGT	CCCGGGAGCA	CATGGGCGAG	TCCCTGAGCC	960
TGAAGGCCGG	TGGTGGGGAC	CTGCTGCTGC	CCCCAGCCC	CAAAGTGGAG	AAGAAGGATC	1020
CCAGCCGGA	GAAGGAGTGG	TGGGAGAATG	CGGGGAACAA	AATCTACACC	ATGGCAGCCG	1080
ACAAGACCAT	TTCAAAGTTG	ATGACCGAAT	ACAAAAAGAG	GAAACAGCAG	CACAACCTGT	1140
CCGCGTTCCC	CAAAGAGGTC	AAAGTGGAGA	AGAAAGGAGA	GCCACTGGGT	CCCAGGGGCC	1200
AGGACTCCCC	GCTGCTTCAG	CGTCCCCAGC	ACTTGATGGA	CCAAGGGCAA	ATGCGGCATT	1260
CCTTCAGCGC	AGGCCCCGAG	CTGCTGCGAC	AGGACAAGAG	GCCCCGCTCA	GGCTCCACCG	1320
GGAGCTCCCT	CAGTGTCTCG	GTGAGAGACG	CAGAAGCACA	GATCCAGGCA	TGGACCAACA	1380
TGGTGCTAAC	AGTTCTCAAT	CAGATTGAGA	TTCTCCCAGA	CCAGACCTTC	ACGGCCCTCC	1440
AGCCCCGAGT	GTTCCCCTGC	ATCAGTCAGC	TGACCTGTCA	CGTGACCGAC	ATCAGAGTTC	1500
GCCAGGCTGT	GAGGGAGTGG	CTGGGCAGGG	TGGGCCGTGT	CTATGACATC	ATTGTGTAGC	1560
CGACTCCTGT	TCTACTCTCC	CACCAAATAA	CAGTAGTGAG	GGTTAGAGTC	CTGCCAATAC	1620
AGCTGTTGCA	TTTTCCCCAC	CACTAGCCCC	ACTTAAACTA	CTACTACTGT	CTCAGAGAAC	1680
AGTGTTCCT	AATGTAAAAA	GCCTTTCCAA	CCACTGATCA	GCATTRGGGC	CATACTAAGG	1740
TTTGTATCTA	GATGACACAA	ACGATATTCT	GATTTTGCAC	ATTATTATAG	AAGAATCTAT	1800
AATCCTTGAT	ATGTTTCTAA	CTCTTGAAGT	ATATTTCCCA	GTGCTTTTGC	TTACAGTGTT	1860
GTCCCCAAAT	GGGTCAATTT	CAAGGATTAC	TCATTTGAAA	ACACTATATT	GATCCATTTG	1920
ATCCATCATT	TAAAAAATAA	ATACAATTCC	TAAGGCAATA	TCTGCTGGTA	AGTCAAGCTG	1980
ATAAACACTC	AGACATCTAG	TACCAGGGAT	TATTAATTGG	AGGAAGATTT	ATGGTTATGG	2040
GTCTGGCTGG	GAAGAAGACA	ACTATAAATA	CATATTCTTG	GGTGTCTATA	TCAAGA	2096

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTAATTCC	CGGGTCGACG	AGCTCACTAG	TCGGCGGCCG	CTCTAGAGGA	TCCAAGCTCG	60
GAATTCCG						68

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCGGATAAC AATTTACAC AGGA

24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGTAAAACGA CGGCCAGT

18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CACCAATCAA GAAACCATC

19

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCCAGCCC GCAGTGTTC

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTAGATGACA CAAACGATA

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGGATGACAG AAGCCAGT

18

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAAAAGCA CTGGGAAA

18

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCCAGCCACT CCCTCACAGC

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACTGGCGGT AGAGGTTGG

19

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACAGTTCCAT GCACAGCTTG

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAGGTCAAAG TGGAGAAGAA AGGAG

25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCTGTATTGG CAGGACTCTA ACCC

24

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCCGCCATGG ACCTGCTGCT GGACTCTTAT AG

32

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGGCCGCCC ACAATGATGT CATAGACACG

30

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Arg	Ile	Arg	Ala	Met	Ala	Gln	Gln	Val	Phe	Met	Leu	Asp	Thr	Gln	Cys
1				5					10					15	
Ser	Pro	Lys	Thr	Pro	Asn	Asn	Phe	Asp	His	Ala	Gln	Ser	Cys	Gln	Leu
			20					25					30		
Ile	Ile	Glu	Leu	Pro	Pro	Asp	Glu	Lys	Pro	Asn	Gly	His	Thr	Lys	Lys
		35				40					45				
Ser	Val	Ser	Phe	Arg	Glu	Ile	Val	Val	Ser	Leu	Leu	Ser	His	Gln	Val
	50				55				60						
Leu	Leu	Gln	Asn	Leu	Tyr	Asp	Ile	Leu	Leu	Glu	Glu	Phe	Val	Lys	Gly
65				70				75						80	
Pro	Ser	Pro	Gly	Glu	Glu	Lys	Thr	Ile	Gln	Val	Pro	Glu	Ala	Lys	Leu
			85					90					95		
Ala	Gly	Phe	Leu	Arg	Tyr	Ile	Ser	Met	Gln	Asn	Leu	Ala	Val	Ile	Phe
			100				105						110		


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Asp Leu Leu Leu Asp Ser Tyr Arg Thr Ala Arg Glu Phe Asp Thr Ser
      115      120      125
Pro Gly Leu Lys Cys Leu Leu Lys Lys Val Ser Gly Ile Gly Gly Ala
      130      135      140
Ala Asn Leu Tyr Arg Gln Ser Ala Met Ser Phe Asn Ile Tyr Phe His
      145      150      155      160
Ala Leu Val Cys Ala Val Leu Thr Asn Gln Glu Thr Ile Thr Ala Glu
      165      170      175
Gln Val Lys Lys Val Leu Phe Glu Asp Glu Arg Ser Thr Asp Ser
      180      185      190
Ser Gln Gln Cys Ser Ser Glu Asp Glu Asp Ile Phe Glu Glu Thr Ala
      195      200      205
Gln Val Ser Pro Pro Arg Gly Lys Glu Lys Arg Gln Trp Arg Ala Arg
      210      215      220
Met Pro Leu Leu Ser Val Gln Pro Val Ser Asn Ala Asp Trp Val Trp
      225      230      235      240
Leu Val Lys Arg Leu His Lys Leu Cys Met Glu Leu Cys Asn Asn Tyr
      245      250      255
Ile Gln Met His Leu Asp Leu Glu Asn Cys Met Glu Glu Pro Pro Ile
      260      265      270
Phe Lys Gly Asp Pro Phe Phe Ile Leu Pro Ser Phe Gln Ser Glu Ser
      275      280      285
Ser Thr Pro Ser Thr Gly Gly Phe Ser Gly Lys Glu Thr Pro Ser Glu
      290      295      300
Asp Asp Arg Ser Gln Ser Arg Glu His Met Gly Glu Ser Leu Ser Leu
      305      310      315      320
Lys Ala Gly Gly Gly Asp Leu Leu Leu Pro Pro Ser Pro Lys Val Glu
      325      330      335
Lys Lys Asp Pro Ser Arg Lys Lys Glu Trp Trp Glu Asn Ala Gly Asn
      340      345      350
Lys Ile Tyr Thr Met Ala Ala Asp Lys Thr Ile Ser Lys Leu Met Thr
      355      360      365
Glu Tyr Lys Lys Arg Lys Gln Gln His Asn Leu Ser Ala Phe Pro Lys
      370      375      380
Glu Val Lys Val Glu Lys Lys Gly Glu Pro Leu Gly Pro Arg Gly Gln
      385      390      395      400
Asp Ser Pro Leu Leu Gln Arg Pro Gln His Leu Met Asp Gln Gly Gln
      405      410      415
Met Arg His Ser Phe Ser Ala Gly Pro Glu Leu Leu Arg Gln Asp Lys
      420      425      430
Arg Pro Arg Ser Gly Ser Thr Gly Ser Ser Leu Ser Val Ser Val Arg
      435      440      445
Asp Ala Glu Ala Gln Ile Gln Ala Trp Thr Asn Met Val Leu Thr Val
      450      455      460
Leu Asn Gln Ile Gln Ile Leu Pro Asp Gln Thr Phe Thr Ala Leu Gln
      465      470      475      480
Pro Ala Val Phe Pro Cys Ile Ser Gln Leu Thr Cys His Val Thr Asp
      485      490      495
Ile Arg Val Arg Gln Ala Val Arg Glu Trp Leu Gly Arg Val Gly Arg
      500      505      510
Val Tyr Asp Ile Ile Val
      515

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Glu Asp Asp Glu Arg Ser Thr Asp Ser Ser Gln Gln Cys Ser Ser Glu
 1 5 10 15
 Asp Glu Asp Ile Phe Glu Glu Thr Ala Gln Val Ser Pro Pro Arg Gly
 20 25 30
 Lys Glu Lys Arg Gln Trp Arg Ala Arg
 35 40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Phe Gln Ser Glu Ser Ser Thr Pro Ser Thr Gly Gly Phe Ser Gly
 1 5 10 15
 Lys Glu Thr Pro Ser Glu Asp Asp Arg Ser Gln Ser Arg Glu His Met
 20 25 30
 Gly Glu Ser
 35

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Pro Lys Val Glu Lys Lys Asp Pro Ser Arg Lys Lys Glu Trp Trp
 1 5 10 15
 Glu Asn Ala Gly Asn Lys Ile Tyr Thr Met Ala Ala Asp Lys Thr Ile
 20 25 30
 Ser Lys Leu Met Thr Glu Tyr Lys
 35 40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Pro Leu Gly Pro Arg Gly Gln Asp Ser Pro Leu Leu Gln Arg Pro
 1 5 10 15
 Gln His Leu Met Asp Gln Gly Gln Met Arg His Ser Phe Ser Ala Gly
 20 25 30
 Pro Glu Leu Leu Arg Gln Asp Lys Arg Pro Arg Ser Gly Ser Thr Gly
 35 40 45
 Ser

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1 5 10 15
His His His His His
20